

SCORE Search Results Details for Application 10516759 and Search Result 20081112_112525_us-10-516-759-14_copy_24_81.rup.

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This page gives you Search Results detail for the Application 10516759 and Search Result 20081112_112525_us-10-516-759-14_copy_24_81.rup.

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GenCore version 6.3

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OM protein - protein search, using sw model

Run on: November 12, 2008, 12:10:55 ; Search time 217 Seconds
(without alignments)
516.952 Million cell updates/sec

Title: US-10-516-759-14_COPY_24_81
Perfect score: 350
Sequence: 1 DIKHNRPDRDCVAEGKVCDP.....RNYSRGGVCVTHCNFLNGEP 58

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5939836 seqs, 1934112985 residues

Total number of hits satisfying chosen parameters: 5939836

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_13.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	350	100.0	63	2	Q9NNX2	HUMAN	Q9nnx2 homo sapien

2	350	100.0	1342	1	ERBB3_HUMAN	P21860	homo sapien
3	350	100.0	1342	1	ERBB3_PONPY	Q5rb22	pongo pygma
4	350	100.0	1342	2	A8K6L6_HUMAN	A8k6l6	homo sapien
5	338	96.6	81	2	O75812_HUMAN	O75812	homo sapien
6	335.5	95.9	1336	2	A6QR62_BOVIN	A6qr62	bos taurus
7	305	87.1	1339	1	ERBB3_MOUSE	Q61526	mus musculus
8	304	86.9	1339	1	ERBB3_RAT	Q62799	rattus norv
9	253	72.3	1547	2	Q4RXV8_TETNG	Q4rxv8	tetraodon n
10	245	70.0	1319	2	Q2HZD7_CHICK	Q2hzd7	gallus gall
11	245	70.0	1429	2	Q5G254_DANRE	Q5g254	danio rerio
12	237	67.7	1328	2	P79754_FUGRU	P79754	fugu rubrip
13	229	65.4	1344	2	Q4RW26_TETNG	Q4rw26	tetraodon n
14	212	60.6	552	2	Q53QS8_HUMAN	Q53qs8	homo sapien
15	212	60.6	1308	1	ERBB4_HUMAN	Q15303	homo sapien
16	209	59.7	1275	2	Q5EBY4_DANRE	Q5eby4	danio rerio
17	208	59.4	732	2	Q6UA27_RAT	Q6ua27	rattus norv
18	208	59.4	1292	1	ERBB4_MOUSE	Q61527	mus musculus
19	208	59.4	1308	1	ERBB4_RAT	Q62956	rattus norv
20	207	59.1	1204	2	A5A753_PIG	A5a753	sus scrofa
21	207	59.1	1209	2	Q8MIL8_PIG	Q8mil8	sus scrofa
22	203	58.0	789	2	Q153D7_XENLA	Q153d7	xenopus lae
23	201	57.4	1209	2	Q9QX70_RAT	Q9qx70	rattus norv
24	200	57.1	643	2	Q9ERV6_MOUSE	Q9erv6	mus musculus
25	200	57.1	655	2	Q9WVF5_MOUSE	Q9wvf5	m epidermal
26	200	57.1	1210	1	EGFR_MOUSE	Q01279	mus musculus
27	200	57.1	1210	2	Q5SVE8_MOUSE	Q5sve8	mus musculus
28	200	57.1	1210	2	Q9EP98_MOUSE	Q9ep98	mus musculus
29	200	57.1	1299	2	Q153D9_XENLA	Q153d9	xenopus lae
30	198	56.6	703	1	EGFR_CHICK	P13387	gallus gall
31	197	56.3	559	2	B0VOR6_DANRE	B0vor6	danio rerio
32	193	55.1	1137	2	Q9W6F6_CHICK	Q9w6f6	gallus gall
33	193	55.1	1276	2	Q4PLA4_CHICK	Q4pla4	gallus gall
34	193	55.1	1292	2	Q4PLA5_CHICK	Q4pla5	gallus gall
35	187	53.4	996	2	Q4RQT4_TETNG	Q4qrt4	tetraodon n
36	185	52.9	388	2	A2VCQ7_HUMAN	A2vcq7	homo sapien
37	185	52.9	464	2	Q147T7_HUMAN	Q147t7	homo sapien
38	185	52.9	645	2	Q68GS6_HUMAN	Q68gs6	homo sapien
39	185	52.9	1081	2	Q59FL8_HUMAN	Q59fl8	homo sapien
40	185	52.9	1091	2	Q504U8_HUMAN	Q504u8	homo sapien
41	185	52.9	1210	1	EGFR_HUMAN	P00533	homo sapien
42	185	52.9	1210	2	A8K2T7_HUMAN	A8k2t7	homo sapien
43	185	52.9	1210	2	A9CB80_HUMAN	A9cb80	homo sapien
44	185	52.9	1210	2	Q2TTR7_HUMAN	Q2ttr7	homo sapien
45	182	52.0	1242	2	A8WED5_CANFA	A8wed5	canis famil

ALIGNMENTS

RESULT 1

Q9NNX2_HUMAN

ID Q9NNX2_HUMAN Unreviewed; 63 AA.

AC Q9NNX2;

DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2000, sequence version 1.
 DT 21-AUG-2007, entry version 23.
 DE ErbB-3 (Fragment).
 GN Name=c-erbB-3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98345147; PubMed=9681822; DOI=10.1038/sj.onc.1201866;
 RA Lee H., Maihle N.J.;
 RT "Isolation and characterization of four alternate c-erbB3 transcripts
 RT expressed in ovarian carcinoma-derived cell lines and normal human
 RT tissues.";
 RL Oncogene 16:3243-3252(1998).
 CC -----
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 CC -----
 DR EMBL; U88356; AAF86628.1; -; Genomic_DNA.
 DR UniGene; Hs.118681; -.
 DR HSSP; P21860; 1M6B.
 DR SMR; Q9NNX2; 1-63.
 DR Ensembl; ENSG00000065361; Homo sapiens.
 DR HGNC; HGNC:3431; ERBB3.
 DR ArrayExpress; Q9NNX2; -.
 DR InterPro; IPR006212; Furin_repeat.
 DR SMART; SM00261; FU; 1.
 PE 2: Evidence at transcript level;
 FT NON_TER 1 1
 FT NON_TER 63 63
 SQ SEQUENCE 63 AA; 6825 MW; F687D8FFC4970980 CRC64;

Query Match 100.0%; Score 350; DB 2; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.4e-31;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRRPRDCVAEGKVCDFLCSSGGCWGPGGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 |||
 Db 2 DIKHNRRPRDCVAEGKVCDFLCSSGGCWGPGGQCLSCRNYSRGGVCVTHCNFLNGEP 59

RESULT 2

ERBB3_HUMAN

ID ERBB3_HUMAN Reviewed; 1342 AA.
 AC P21860;
 DT 01-MAY-1991, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1991, sequence version 1.
 DT 08-APR-2008, entry version 99.
 DE Receptor tyrosine-protein kinase erbB-3 precursor (EC 2.7.10.1) (c-
 DE erbB3) (Tyrosine kinase-type cell surface receptor HER3).
 GN Name=ERBB3; Synonyms=HER3;

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RX MEDLINE=90083234; PubMed=2687875;
 RA Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A.;
 RT "Isolation and characterization of ERBB3, a third member of the
 RT ERBB/epidermal growth factor receptor family: evidence for
 RT overexpression in a subset of human mammary tumors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RX MEDLINE=90311312; PubMed=2164210;
 RA Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L.,
 RA Todaro G.J., Shoyab M.;
 RT "Molecular cloning and expression of an additional epidermal growth
 RT factor receptor-related gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
 RC TISSUE=Placenta;
 RX MEDLINE=93282822; PubMed=7685162; DOI=10.1006/bbrc.1993.1542;
 RA Katoh M., Yazaki Y., Sugimura T., Terada M.;
 RT "c-erbB3 gene encodes secreted as well as transmembrane receptor
 RT tyrosine kinase.";
 RL Biochem. Biophys. Res. Commun. 192:1189-1197(1993).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Skin;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 RT project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 RN [5]
 RP INTERACTION WITH PA2G4.
 RX PubMed=11325528; DOI=10.1016/S0303-7207(01)00387-2;
 RA Lessor T.J., Hamburger A.W.;
 RT "Regulation of the ErbB3 binding protein Ebp1 by protein kinase C.";
 RL Mol. Cell. Endocrinol. 175:185-191(2001).
 RN [6]
 RP INTERACTION WITH MUC1.
 RX PubMed=12939402;
 RA Li Y., Yu W.-H., Ren J., Chen W., Huang L., Kharbanda S., Loda M.,
 RA Kufe D.;
 RT "Heregulin targets gamma-catenin to the nucleolus by a mechanism
 RT dependent on the DF3/MUC1 oncoprotein.";
 RL Mol. Cancer Res. 1:765-775(2003).
 RN [7]
 RP INTERACTION WITH CSPG5, AND FUNCTION.
 RX PubMed=15358134; DOI=10.1016/j.bbrc.2004.07.066;

RA Kinugasa Y., Ishiguro H., Tokita Y., Oohira A., Ohmoto H.,
RA Higashiyama S.;
RT "Neuroglycan C, a novel member of the neuregulin family.";
RL Biochem. Biophys. Res. Commun. 321:1045-1049(2004).
RN [8]
RP INVOLVEMENT IN LCCS2.
RX PubMed=17701904; DOI=10.1086/520770;
RA Narkis G., Ofir R., Manor E., Landau D., Elbedour K., Birk O.S.;
RT "Lethal congenital contractural syndrome type 2 (LCCS2) is caused by a
RT mutation in ERBB3 (Her3), a modulator of the phosphatidylinositol-3-
RT kinase/Akt pathway.";
RL Am. J. Hum. Genet. 81:589-595(2007).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 20-640, DISULFIDE BONDS, AND
RP GLYCOSYLATION AT ASN-250; ASN-353; ASN-408; ASN-414; ASN-437; ASN-469;
RP ASN-522 AND ASN-566.
RX PubMed=12154198; DOI=10.1126/science.1074611;
RA Cho H.S., Leahy D.J.;
RT "Structure of the extracellular region of HER3 reveals an interdomain
RT tether.";
RL Science 297:1330-1333(2002).
RN [10]
RP VARIANTS [LARGE SCALE ANALYSIS] TYR-20; LEU-30; MET-104; ILE-204;
RP TRP-683; LEU-717; THR-744; ARG-998; CYS-1119; HIS-1127; ILE-1177 AND
RP LYS-1254.
RX PubMed=17344846; DOI=10.1038/nature05610;
RA Greenman C., Stephens P., Smith R., Dalgliesh G.L., Hunter C.,
RA Bignell G., Davies H., Teague J., Butler A., Stevens C., Edkins S.,
RA O'Meara S., Vastrik I., Schmidt E.E., Avis T., Barthorpe S.,
RA Bhamra G., Buck G., Choudhury B., Clements J., Cole J., Dicks E.,
RA Forbes S., Gray K., Halliday K., Harrison R., Hills K., Hinton J.,
RA Jenkinson A., Jones D., Menzies A., Mironenko T., Perry J., Raine K.,
RA Richardson D., Shepherd R., Small A., Tofts C., Varian J., Webb T.,
RA West S., Widawski S., Yates A., Cahill D.P., Louis D.N., Goldstraw P.,
RA Nicholson A.G., Brasseur F., Looijenga L., Weber B.L., Chiew Y.-E.,
RA DeFazio A., Greaves M.F., Green A.R., Campbell P., Birney E.,
RA Easton D.F., Chenevix-Trench G., Tan M.-H., Khoo S.K., Teh B.T.,
RA Yuen S.T., Leung S.Y., Wooster R., Futreal P.A., Stratton M.R.;
RT "Patterns of somatic mutation in human cancer genomes.";
RL Nature 446:153-158(2007).
CC -!- FUNCTION: Binds and is activated by neuregulins and NTAK.
CC -!- CATALYTIC ACTIVITY: ATP + a [protein]-L-tyrosine = ADP + a
CC [protein]-L-tyrosine phosphate.
CC -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC (Potential). Interacts with CSPG5, PA2G4 and MUC1.
CC -!- INTERACTION:
CC P00533:EGFR; NbExp=2; IntAct=EBI-720706, EBI-297353;
CC P04626:ERBB2; NbExp=4; IntAct=EBI-720706, EBI-641062;
CC Q15303:ERBB4; NbExp=2; IntAct=EBI-720706, EBI-80371;
CC Q9UQ80:PA2G4; NbExp=1; IntAct=EBI-720706, EBI-924893;
CC P27986:PIK3R1; NbExp=3; IntAct=EBI-720706, EBI-79464;
CC -!- SUBCELLULAR LOCATION: Isoform 1: Cell membrane; Single-pass type I
CC membrane protein.
CC -!- SUBCELLULAR LOCATION: Isoform 2: Secreted.

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CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=2;
CC          Name=1; Synonyms=long form;
CC          IsoId=P21860-1; Sequence=Displayed;
CC          Name=2; Synonyms=short form;
CC          IsoId=P21860-2; Sequence=VSP_002893, VSP_002894;
CC      -!- TISSUE SPECIFICITY: Epithelial tissues and brain.
CC      -!- DOMAIN: The cytoplasmic part of the receptor may interact with the
CC          SH2 or SH3 domains of many signal-transducing proteins.
CC      -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC          and promotes its association with the p85 subunit of
CC          phosphatidylinositol 3-kinase (By similarity).
CC      -!- DISEASE: Overexpressed in a subset of human mammary tumors.
CC      -!- DISEASE: Defects in ERBB3 are the cause of lethal congenital
CC          contracture syndrome type 2 (LCCS2) [MIM:607598]; also called
CC          Israeli Bedouin multiple contracture syndrome type A. LCCS2 is an
CC          autosomal recessive neurogenic form of a neonatally lethal
CC          arthrogryposis that is associated with atrophy of the anterior
CC          horn of the spinal cord. The LCCS2 syndrome is characterized by
CC          multiple joint contractures, anterior horn atrophy in the spinal
CC          cord, and a unique feature of a markedly distended urinary
CC          bladder. The phenotype suggests a spinal cord neuropathic
CC          etiology.
CC      -!- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein
CC          kinase family. EGF receptor subfamily.
CC      -!- SIMILARITY: Contains 1 protein kinase domain.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC      -----
DR      EMBL; M29366; AAA35790.1; -; mRNA.
DR      EMBL; M34309; AAA35979.1; -; mRNA.
DR      EMBL; S61953; AAB26935.1; -; mRNA.
DR      EMBL; BC082992; AAH82992.1; -; mRNA.
DR      PIR; A36223; A36223.
DR      PIR; JH0803; JH0803.
DR      RefSeq; NP_001005915.1; -.
DR      RefSeq; NP_001973.2; -.
DR      UniGene; Hs.118681; -.
DR      PDB; 1M6B; X-ray; 2.60 A; A/B=20-640.
DR      PDBsum; 1M6B; -.
DR      DIP; DIP:511N; -.
DR      DIP; DIP:6093N; -.
DR      DIP; DIP:94N; -.
DR      IntAct; P21860; -.
DR      PhosphoSite; P21860; -.
DR      Ensembl; ENSG00000065361; Homo sapiens.
DR      GeneID; 2065; -.
DR      H-InvDB; HIX0010715; -.
DR      HGNC; HGNC:3431; ERBB3.
DR      HPA; CAB000088; -.
DR      MIM; 190151; gene.
DR      MIM; 607598; phenotype.
DR      PharmGKB; PA27846; -.

```

DR ArrayExpress; P21860; -.

DR CleanEx; HS_ERBB3; -.

DR GermOnline; ENSG00000065361; Homo sapiens.

DR GO; GO:0016323; C:basolateral plasma membrane; IDA:UniProtKB.

DR GO; GO:0005615; C:extracellular space; IDA:UniProtKB.

DR GO; GO:0005887; C:integral to plasma membrane; TAS:ProtInc.

DR GO; GO:0043235; C:receptor complex; ISS:UniProtKB.

DR GO; GO:0019838; F:growth factor binding; IPI:UniProtKB.

DR GO; GO:0046982; F:protein heterodimerization activity; IDA:UniProtKB.

DR GO; GO:0042803; F:protein homodimerization activity; NAS:UniProtKB.

DR GO; GO:0030296; F:protein tyrosine kinase activator activity; IDA:UniProtKB.

DR GO; GO:0004888; F:transmembrane receptor activity; ISS:UniProtKB.

DR GO; GO:0021545; P:cranial nerve development; ISS:UniProtKB.

DR GO; GO:0007507; P:heart development; ISS:UniProtKB.

DR GO; GO:0007162; P:negative regulation of cell adhesion; IDA:UniProtKB.

DR GO; GO:0043524; P:negative regulation of neuron apoptosis; ISS:UniProtKB.

DR GO; GO:0051048; P:negative regulation of secretion; IDA:UniProtKB.

DR GO; GO:0009968; P:negative regulation of signal transduction; IDA:UniProtKB.

DR GO; GO:0014068; P:positive regulation of phosphoinositide 3-k. . .; TAS:UniProtKB.

DR GO; GO:0042127; P:regulation of cell proliferation; IDA:UniProtKB.

DR GO; GO:0014037; P:Schwann cell differentiation; ISS:UniProtKB.

DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS:UniProtKB.

DR GO; GO:0042060; P:wound healing; NAS:UniProtKB.

DR InterPro; IPR000494; EGF_rcpt_L.

DR InterPro; IPR006211; Furin-like.

DR InterPro; IPR006212; Furin_repeat.

DR InterPro; IPR000719; Prot_kinase_core.

DR InterPro; IPR016245; Tyr_kinase_rcpt_EGF/ERB/XmrK.

DR InterPro; IPR001245; Tyr_pkinase.

DR InterPro; IPR008266; Tyr_pkinase_AS.

Query Match 100.0%; Score 350; DB 1; Length 1342;
 Best Local Similarity 100.0%; Pred. No. 2.5e-30;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRPRRDCAEGKVCDPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 483 DIKHNRPRRDCAEGKVCDPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

RESULT 3

ERBB3_PONPY

ID ERBB3_PONPY Reviewed; 1342 AA.

AC Q5RB22;

DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.

DT 21-DEC-2004, sequence version 1.

DT 08-APR-2008, entry version 28.

DE Receptor tyrosine-protein kinase erbB-3 precursor (EC 2.7.10.1).

GN Name=ERBB3;

OS Pongo pygmaeus (Bornean orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Hominidae; Pongo.

OX NCBI_TaxID=9600;

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RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC      TISSUE=Kidney;
RG      The German cDNA consortium;
RL      Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC      -!- FUNCTION: Binds and is activated by neuregulins and NTAK. May also
CC      be activated by CSPG5 (By similarity).
CC      -!- CATALYTIC ACTIVITY: ATP + a [protein]-L-tyrosine = ADP + a
CC      [protein]-L-tyrosine phosphate.
CC      -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC      (Potential). Interacts with CSPG5, PA2G4 and MUC1 (By similarity).
CC      -!- SUBCELLULAR LOCATION: Membrane; Single-pass type I membrane
CC      protein (By similarity).
CC      -!- DOMAIN: The cytoplasmic part of the receptor may interact with the
CC      SH2 or SH3 domains of many signal-transducing proteins.
CC      -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC      and promotes its association with the p85 subunit of
CC      phosphatidylinositol 3-kinase (By similarity).
CC      -!- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein
CC      kinase family. EGF receptor subfamily.
CC      -!- SIMILARITY: Contains 1 protein kinase domain.
CC      -----
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CC      -----
DR      EMBL; CR858836; CAH91038.1; -, mRNA.
DR      InterPro; IPR000494; EGF_rcpt_L.
DR      InterPro; IPR006211; Furin-like.
DR      InterPro; IPR006212; Furin_repeat.
DR      InterPro; IPR000719; Prot_kinase_core.
DR      InterPro; IPR016245; Tyr_kinase_rcpt_EGF/ERB/XmrK.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      InterPro; IPR008266; Tyr_pkinase_AS.
DR      Pfam; PF00757; Furin-like; 1.
DR      Pfam; PF07714; Pkinase_Tyr; 1.
DR      Pfam; PF01030; Recep_L_domain; 2.
DR      PIRSF; PIRSF000619; TyrPK_EGF-R; 1.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00261; FU; 5.
DR      SMART; SM00219; TyrKc; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR      PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00109; PROTEIN_KINASE_TYR; FALSE_NEG.
PE      2: Evidence at transcript level;
KW      ATP-binding; Glycoprotein; Kinase; Membrane; Nucleotide-binding;
KW      Phosphoprotein; Receptor; Signal; Transferase; Transmembrane;
KW      Tyrosine-protein kinase.
FT      SIGNAL          1      19      Potential.
FT      CHAIN           20     1342    Receptor tyrosine-protein kinase erbB-3
FT                                     (By similarity).
FT                                     /FTId=PRO_0000042232.
FT      TOPO_DOM        20      641    Extracellular (Potential).
FT      TRANSMEM        642     664    Potential.

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FT	TOPO_DOM	665	1342	Cytoplasmic (Potential).
FT	DOMAIN	709	966	Protein kinase.
FT	NP_BIND	715	723	ATP (By similarity).
FT	ACT_SITE	834	834	Proton acceptor (By similarity).
FT	BINDING	742	742	ATP (By similarity).
FT	CARBOHYD	126	126	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	250	250	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	353	353	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	408	408	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	414	414	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	437	437	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	469	469	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	522	522	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	566	566	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	616	616	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID	186	194	By similarity.
FT	DISULFID	190	202	By similarity.
FT	DISULFID	210	218	By similarity.
FT	DISULFID	214	226	By similarity.
FT	DISULFID	227	235	By similarity.
FT	DISULFID	231	243	By similarity.
FT	DISULFID	246	255	By similarity.
FT	DISULFID	259	286	By similarity.
FT	DISULFID	290	301	By similarity.
FT	DISULFID	305	320	By similarity.
FT	DISULFID	323	327	By similarity.
FT	DISULFID	500	509	By similarity.
FT	DISULFID	504	517	By similarity.
FT	DISULFID	520	529	By similarity.
FT	DISULFID	533	549	By similarity.
FT	DISULFID	552	565	By similarity.
FT	DISULFID	556	573	By similarity.
FT	DISULFID	576	585	By similarity.
FT	DISULFID	589	610	By similarity.
FT	DISULFID	613	621	By similarity.
FT	DISULFID	617	629	By similarity.
SQ	SEQUENCE	1342 AA;	148104 MW;	F7FB7E27C573916D CRC64;

Query Match 100.0%; Score 350; DB 1; Length 1342;
 Best Local Similarity 100.0%; Pred. No. 2.5e-30;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRRPRRDCAVEGKVCDDLPCSSGGCWGPGGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 483 DIKHNRRPRRDCAVEGKVCDDLPCSSGGCWGPGGQCLSCRNYSRGGVCVTHCNFLNGEP 540

RESULT 4

A8K6L6_HUMAN

ID A8K6L6_HUMAN Unreviewed; 1342 AA.

AC A8K6L6;

DT 04-DEC-2007, integrated into UniProtKB/TrEMBL.

DT 04-DEC-2007, sequence version 1.

DT 08-APR-2008, entry version 4.

DE cDNA FLJ76884, highly similar to Homo sapiens v-erb-b2 erythroblastic
 DE leukemia viral oncogene homolog 3 (avian) (ERBB3), transcript variant
 DE 1, mRNA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RA Wakamatsu A., Yamamoto J., Kimura K., Ishii S., Watanabe K.,
 RA Sugiyama A., Murakawa K., Kaida T., Tsuchiya K., Fukuzumi Y.,
 RA Kumagai A., Oishi Y., Yamamoto S., Ono Y., Komori Y., Yamazaki M.,
 RA Kisu Y., Nishikawa T., Sugano S., Nomura N., Isogai T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (OCT-2007) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 DR EMBL; AK291681; BAF84370.1; -; mRNA.
 DR UniGene; Hs.118681; -.
 DR GO; GO:0016020; C:membrane; IEA:InterPro.
 DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA:InterPro.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
 DR InterPro; IPR000494; EGF_rcpt_L.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin_repeat.
 DR InterPro; IPR000719; Prot_kinase_core.
 DR InterPro; IPR016245; Tyr_kinase_rcpt_EGF/ERB/XmrK.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PIRSF; PIRSF000619; TyrPK_EGF-R; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU; 5.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 PE 2: Evidence at transcript level;
 SQ SEQUENCE 1342 AA; 148070 MW; 333FA8D7B3A39631 CRC64;

Query Match 100.0%; Score 350; DB 2; Length 1342;
 Best Local Similarity 100.0%; Pred. No. 2.5e-30;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRRPRRDCAVAGKVCDDLCSGGCGWPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 483 DIKHNRRPRRDCAVAGKVCDDLCSGGCGWPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

DE ERBB3 protein.
GN Name=ERBB3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=L1 Hereford; TISSUE=Fetal skin;
RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL Submitted (JUL-2007) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC150128; AAI50129.1; -; mRNA.
DR RefSeq; NP_001096575.1; -.
DR UniGene; Bt.64779; -.
DR GeneID; 785655; -.
DR KEGG; bta:785655; -.
DR GO; GO:0016020; C:membrane; IEA:InterPro.
DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA:InterPro.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
DR InterPro; IPR000494; EGF_rcpt_L.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR000719; Prot_kinase_core.
DR InterPro; IPR016245; Tyr_kinase_rcpt_EGF/ERB/XmrK.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PIRSF; PIRSF000619; TyrPK_EGF-R; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 5.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PE 2; Evidence at transcript level;
SQ SEQUENCE 1336 AA; 147581 MW; A1DCB7ED159799FC CRC64;

Query Match 95.9%; Score 335.5; DB 2; Length 1336;
Best Local Similarity 98.3%; Pred. No. 1.1e-28;
Matches 57; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DIKHNRPRRDCAEGKVCDDPLCSSGGCGWPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58

Db 483 DIKHNRPRRDCVAEGKVCDDLPC-SGGCWGPGPGQCLSCRNYSGRGVCVTCNLFNGEP 539

RESULT 7

ERBB3_MOUSE

ID ERBB3_MOUSE Reviewed; 1339 AA.

AC Q61526; Q3KQR1; Q68J64; Q810U8; Q8K317;

DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.

DT 11-OCT-2005, sequence version 2.

DT 08-APR-2008, entry version 71.

DE Receptor tyrosine-protein kinase erbB-3 precursor (EC 2.7.10.1) (c-erbB3) (Glial growth factor receptor).

GN Name=ErbB3;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC STRAIN=BALB/c;

RA Yamauchi J., Shooter E.M.;

RT "Involvement of the ErbB3 signaling pathway in Schwann cell migration.";

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=FVB/N; TISSUE=Mammary tumor, and Thyroid;

RX PubMed=15489334; DOI=10.1101/gr.2596504;

RG The MGC Project Team;

RT "The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC).";

RL Genome Res. 14:2121-2127(2004).

RN [3]

RP NUCLEOTIDE SEQUENCE [MRNA] OF 1061-1154.

RC TISSUE=Muscle fibroblast;

RX MEDLINE=96069911; PubMed=7589796; DOI=10.1006/dbio.1995.0012;

RA Moscoso L.M., Chu G.C., Gautam M., Noakes P.G., Merlie J.P., Sanes J.R.;

RT "Synapse-associated expression of an acetylcholine receptor-inducing protein, ARIA/hergulin, and its putative receptors, ErbB2 and ErbB3, in developing mammalian muscle.";

RL Dev. Biol. 172:158-169(1995).

CC -!- FUNCTION: Binds and is activated by neuregulins and NTAK. May also be activated by CSPG5 (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + a [protein]-L-tyrosine = ADP + a [protein]-L-tyrosine phosphate.

CC -!- SUBUNIT: Heterodimer with each of the other ERBB receptors (Potential). Interacts with CSPG5, PA2G4 and MUC1 (By similarity).

CC -!- INTERACTION:

CC Q9UQ80:PA2G4 (xeno); NbExp=1; IntAct=EBI-931878, EBI-924893;

CC -!- SUBCELLULAR LOCATION: Membrane; Single-pass type I membrane protein (By similarity).

```

CC      -!- TISSUE SPECIFICITY: In the muscle, expression localizes to the
CC      synaptic sites of muscle fibers.
CC      -!- DOMAIN: The cytoplasmic part of the receptor may interact with the
CC      SH2 or SH3 domains of many signal-transducing proteins.
CC      -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC      and promotes its association with the p85 subunit of
CC      phosphatidylinositol 3-kinase (By similarity).
CC      -!- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein
CC      kinase family. EGF receptor subfamily.
CC      -!- SIMILARITY: Contains 1 protein kinase domain.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AY686636; AAT95433.1; -; mRNA.
DR      EMBL; BC029028; AAH29028.1; -; mRNA.
DR      EMBL; BC049279; AAH49279.1; -; mRNA.
DR      EMBL; BC106091; AAI06092.1; -; mRNA.
DR      EMBL; L47240; AAA93533.1; -; mRNA.
DR      RefSeq; NP_034283.1; -.
DR      UniGene; Mm.373043; -.
DR      HSSP; Q9H2C9; 1M14.
DR      IntAct; Q61526; -.
DR      PhosphoSite; Q61526; -.
DR      Ensembl; ENSMUSG00000018166; Mus musculus.
DR      GeneID; 13867; -.
DR      KEGG; mmu:13867; -.
DR      MGI; MGI:95411; Erbb3.
DR      ArrayExpress; Q61526; -.
DR      GermOnline; ENSMUSG00000018166; Mus musculus.
DR      GO; GO:0016324; C:apical plasma membrane; IDA:MGI.
DR      GO; GO:0016328; C:lateral plasma membrane; IDA:MGI.
DR      GO; GO:0005515; F:protein binding; IPI:UniProtKB.
DR      GO; GO:0021545; P:cranial nerve development; IMP:MGI.
DR      GO; GO:0007507; P:heart development; IMP:MGI.
DR      GO; GO:0043524; P:negative regulation of neuron apoptosis; IMP:MGI.
DR      GO; GO:0014037; P:Schwann cell differentiation; IMP:MGI.
DR      InterPro; IPR000494; EGF_rcpt_L.
DR      InterPro; IPR006211; Furin-like.
DR      InterPro; IPR006212; Furin_repeat.
DR      InterPro; IPR000719; Prot_kinase_core.
DR      InterPro; IPR016245; Tyr_kinase_rcpt_EGF/ERB/XmrK.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      InterPro; IPR008266; Tyr_pkinase_AS.
DR      Pfam; PF00757; Furin-like; 1.
DR      Pfam; PF07714; Pkinase_Tyr; 1.
DR      Pfam; PF01030; Recep_L_domain; 2.
DR      PIRSF; PIRSF000619; TyrPK_EGF-R; 1.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00261; FU; 5.
DR      SMART; SM00219; TyrKc; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR      PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

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DR  PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PE  1: Evidence at protein level;
KW  ATP-binding; Glycoprotein; Kinase; Membrane; Nucleotide-binding;
KW  Phosphoprotein; Receptor; Signal; Transferase; Transmembrane;
KW  Tyrosine-protein kinase.
FT  SIGNAL          1      19      Potential.
FT  CHAIN           20     1339    Receptor tyrosine-protein kinase erbB-3.
FT                                     /FTId=PRO_0000042231.
FT  TOPO_DOM        20     641     Extracellular (Potential).
FT  TRANSMEM        642     662     Potential.
FT  TOPO_DOM        663     1339    Cytoplasmic (Potential).
FT  DOMAIN          707     964     Protein kinase.
FT  NP_BIND         713     721     ATP (By similarity).
FT  ACT_SITE        832     832     Proton acceptor (By similarity).
FT  BINDING         740     740     ATP (By similarity).
FT  CARBOHYD        126     126     N-linked (GlcNAc. . .) (Potential).
FT  CARBOHYD        250     250     N-linked (GlcNAc. . .) (Potential).
FT  CARBOHYD        353     353     N-linked (GlcNAc. . .) (Potential).
FT  CARBOHYD        408     408     N-linked (GlcNAc. . .) (Potential).
FT  CARBOHYD        414     414     N-linked (GlcNAc. . .) (Potential).
FT  CARBOHYD        437     437     N-linked (GlcNAc. . .) (Potential).
FT  CARBOHYD        469     469     N-linked (GlcNAc. . .) (Potential).
FT  CARBOHYD        522     522     N-linked (GlcNAc. . .) (Potential).
FT  CARBOHYD        566     566     N-linked (GlcNAc. . .) (Potential).
FT  CARBOHYD        616     616     N-linked (GlcNAc. . .) (Potential).
FT  DISULFID        186     194     By similarity.
FT  DISULFID        190     202     By similarity.
FT  DISULFID        210     218     By similarity.
FT  DISULFID        214     226     By similarity.
FT  DISULFID        227     235     By similarity.
FT  DISULFID        231     243     By similarity.
FT  DISULFID        246     255     By similarity.
FT  DISULFID        259     286     By similarity.
FT  DISULFID        290     301     By similarity.
FT  DISULFID        305     320     By similarity.
FT  DISULFID        323     327     By similarity.
FT  DISULFID        500     509     By similarity.
FT  DISULFID        504     517     By similarity.
FT  DISULFID        520     529     By similarity.
FT  DISULFID        533     549     By similarity.
FT  DISULFID        552     565     By similarity.
FT  DISULFID        556     573     By similarity.
FT  DISULFID        576     585     By similarity.
FT  DISULFID        589     610     By similarity.
FT  DISULFID        613     621     By similarity.
FT  DISULFID        617     629     By similarity.
FT  CONFLICT        1067    1067     A -> V (in Ref. 3; AAA93533).
SQ  SEQUENCE        1339 AA;  147613 MW;  59D56FD9C9536FBE CRC64;

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Query Match 87.1%; Score 305; DB 1; Length 1339;
 Best Local Similarity 87.9%; Pred. No. 3e-25;
 Matches 51; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIKHNRPRRDCAEGKVCDPLCSSGGCGWPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58

Db 483 DIKYNRPLGECVAEGKVCDDLPLCSSGGCGWPGPGQCLSCRNYSREGVCVTHCNVLQGEF 540

RESULT 8

ERBB3_RAT

ID ERBB3_RAT Reviewed; 1339 AA.

AC Q62799; Q62955;

DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.

DT 06-JUN-2002, sequence version 3.

DT 08-APR-2008, entry version 77.

DE Receptor tyrosine-protein kinase erbB-3 precursor (EC 2.7.10.1) (c-erbB3).

GN Name=ErbB3;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC STRAIN=Sprague-Dawley; TISSUE=Liver;

RX MEDLINE=96096535; PubMed=8522190; DOI=10.1016/0378-1119(95)00436-A;

RA Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland J.G.;

RT "Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.";

RL Gene 165:279-284(1995).

RN [2]

RP SEQUENCE REVISION TO 85; 513 AND 565.

RA Hellyer N.J., Koland J.G.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE [MRNA] OF 922-1097.

RC STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;

RX MEDLINE=97184212; PubMed=9030624;

RA Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

RT "Expression of neuregulins and their putative receptors, ErbB2 and ErbB3, is induced during Wallerian degeneration.";

RL J. Neurosci. 17:1642-1659(1997).

CC -!- FUNCTION: Binds and is activated by neuregulins and NTAK. May also be activated by CSPG5.

CC -!- CATALYTIC ACTIVITY: ATP + a [protein]-L-tyrosine = ADP + a [protein]-L-tyrosine phosphate.

CC -!- SUBUNIT: Heterodimer with each of the other ERBB receptors (Potential). Interacts with CSPG5, PA2G4 and MUC1 (By similarity).

CC -!- SUBCELLULAR LOCATION: Membrane; Single-pass type I membrane protein.

CC -!- DOMAIN: The cytoplasmic part of the receptor may interact with the SH2 or SH3 domains of many signal-transducing proteins.

CC -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues and promotes its association with the p85 subunit of phosphatidylinositol 3-kinase.

CC -!- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein kinase family. EGF receptor subfamily.


```

CC      -!- SIMILARITY: Contains 1 protein kinase domain.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; U29339; AAC28498.2; -; mRNA.
DR      EMBL; U52530; AAC53050.1; -; mRNA.
DR      PIR; JC4387; JC4387.
DR      RefSeq; NP_058914.2; -.
DR      UniGene; Rn.10228; -.
DR      HSSP; P21860; 1M6B.
DR      PhosphoSite; Q62799; -.
DR      Ensembl; ENSRNOG00000004964; Rattus norvegicus.
DR      GeneID; 29496; -.
DR      KEGG; rno:29496; -.
DR      RGD; 69323; Erbb3.
DR      ArrayExpress; Q62799; -.
DR      GermOnline; ENSRNOG00000004964; Rattus norvegicus.
DR      InterPro; IPR000494; EGF_rcpt_L.
DR      InterPro; IPR006211; Furin-like.
DR      InterPro; IPR006212; Furin_repeat.
DR      InterPro; IPR000719; Prot_kinase_core.
DR      InterPro; IPR016245; Tyr_kinase_rcpt_EGF/ERB/XmrK.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      InterPro; IPR008266; Tyr_pkinase_AS.
DR      Pfam; PF00757; Furin-like; 1.
DR      Pfam; PF07714; Pkinase_Tyr; 1.
DR      Pfam; PF01030; Recep_L_domain; 2.
DR      PIRSF; PIRSF000619; TyrPK_EGF-R; 1.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00261; FU; 5.
DR      SMART; SM00219; TyrKc; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR      PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PE      2: Evidence at transcript level;
KW      ATP-binding; Glycoprotein; Kinase; Membrane; Nucleotide-binding;
KW      Phosphoprotein; Receptor; Signal; Transferase; Transmembrane;
KW      Tyrosine-protein kinase.
FT      SIGNAL          1           19           Potential.
FT      CHAIN           20          1339         Receptor tyrosine-protein kinase erbB-3.
FT                                          /FTId=PRO_0000016673.
FT      TOPO_DOM        20          643         Extracellular (Potential).
FT      TRANSMEM        644          662         Potential.
FT      TOPO_DOM        663          1339        Cytoplasmic (Potential).
FT      DOMAIN          707          964         Protein kinase.
FT      NP_BIND         713          721         ATP (By similarity).
FT      COMBIAS         183          259         Cys-rich.
FT      ACT_SITE        832          832         Proton acceptor (By similarity).
FT      BINDING         740          740         ATP (By similarity).
FT      CARBOHYD        126          126         N-linked (GlcNAc... ) (Potential).
FT      CARBOHYD        250          250         N-linked (GlcNAc... ) (Potential).
FT      CARBOHYD        353          353         N-linked (GlcNAc... ) (Potential).

```

FT	CARBOHYD	408	408	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	414	414	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	437	437	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	469	469	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	522	522	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	566	566	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	616	616	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID	186	194	By similarity.
FT	DISULFID	190	202	By similarity.
FT	DISULFID	210	218	By similarity.
FT	DISULFID	214	226	By similarity.
FT	DISULFID	227	235	By similarity.
FT	DISULFID	231	243	By similarity.
FT	DISULFID	246	255	By similarity.
FT	DISULFID	259	286	By similarity.
FT	DISULFID	290	301	By similarity.
FT	DISULFID	305	320	By similarity.
FT	DISULFID	323	327	By similarity.
FT	DISULFID	500	509	By similarity.
FT	DISULFID	504	517	By similarity.
FT	DISULFID	520	529	By similarity.
FT	DISULFID	533	549	By similarity.
FT	DISULFID	556	573	By similarity.
FT	DISULFID	576	585	By similarity.
FT	DISULFID	589	610	By similarity.
FT	DISULFID	613	621	By similarity.
FT	DISULFID	617	629	By similarity.
FT	CONFLICT	1028	1028	L -> P (in Ref. 3; AAC53050).
SQ	SEQUENCE	1339	AA; 147546	MW; 0AA5F2402BBFDF1E CRC64;

Query Match 86.9%; Score 304; DB 1; Length 1339;
 Best Local Similarity 86.2%; Pred. No. 3.9e-25;
 Matches 50; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIKHNRRPRDCVAEGKVCDDLPCSSGGCWGPQGCLSCRNYSRGGVCVTHCNFLNGEP 58
 |||::|| :|:||||||||||||||||||||||||||| ||||| |||
 Db 483 DIKYDRPLGECLAEGKVCDDLPCSSGGCWGPQGCLSCRNYSREGVCVTHCNFLQGEF 540

RESULT 9

Q4RXV8_TETNG

ID Q4RXV8_TETNG Unreviewed; 1547 AA.
 AC Q4RXV8;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 08-APR-2008, entry version 18.
 DE Chromosome 11 SCAF14979, whole genome shotgun sequence. (Fragment).
 GN ORFNames=GSTENG00027265001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontoidea; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;

```

RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=15496914; DOI=10.1038/nature03025;
RA      Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA      Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA      Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA      Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA      Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA      Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA      Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA      Parra G., Lardier G., Chapple P., McKernan K.J., McEwan P., Bosak S.,
RA      Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA      Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA      Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA      Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT      "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT      the early vertebrate proto-karyotype.";
RL      Nature 431:946-957(2004).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RG      Genoscope; Whitehead Institute Centre for Genome Research;
RL      Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein
CC      kinase family.
CC      -!- CAUTION: The sequence shown here is derived from an
CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; CAAE01014979; CAG06774.1; -; Genomic_DNA.
DR      GO; GO:0016020; C:membrane; IEA:InterPro.
DR      GO; GO:0005524; F:ATP binding; IEA:InterPro.
DR      GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IEA:InterPro.
DR      GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
DR      InterPro; IPR000494; EGF_rcpt_L.
DR      InterPro; IPR006211; Furin-like.
DR      InterPro; IPR006212; Furin_repeat.
DR      InterPro; IPR000719; Prot_kinase_core.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      Pfam; PF00757; Furin-like; 1.
DR      Pfam; PF07714; Pkinase_Tyr; 2.
DR      Pfam; PF01030; Recep_L_domain; 2.
DR      ProDom; PD0000001; Prot_kinase; 2.
DR      SMART; SM00261; FU; 4.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PE      3: Inferred from homology;
KW      ATP-binding; Nucleotide-binding; Tyrosine-protein kinase.
FT      NON_TER      1      1
SQ      SEQUENCE      1547 AA; 171198 MW; 33EAB6CEB1C29324 CRC64;

```

Query Match 72.3%; Score 253; DB 2; Length 1547;

Best Local Similarity 73.7%; Pred. No. 2.6e-19;
Matches 42; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIKHNRRPRRDVAEGKVCDDLPCSSGGCWGPQGLSCRNYSRGGVCVTHCNFLNGE 57
||| |||| ||| | |||||| |||||| ||||: ||||:| | || |:
Db 520 DIKDNRRPSDCVRENFCDDLPCSSDGCWGPQGLSCKKYSRGGICVADCMFLAGD 576

RESULT 10

Q2HZD7_CHICK

ID Q2HZD7_CHICK Unreviewed; 1319 AA.

AC Q2HZD7;

DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.

DT 07-MAR-2006, sequence version 1.

DT 08-APR-2008, entry version 16.

DE Receptor tyrosine-protein kinase.

GN Name=erbB3;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Dinosauria; Saurischia; Theropoda; Coelurosauria; Aves;

OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Wang Y., Li J., Leung F.C.;

RT "Cloning of Chicken erbB-3 and Characterization of its Expression in
RT the Chicken Ovary.";

RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.

CC

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CC

DR EMBL; DQ358720; ABC88378.1; -; mRNA.

DR RefSeq; NP_001038134.1; -.

DR UniGene; Gga.33709; -.

DR GeneID; 693245; -.

DR KEGG; gga:693245; -.

DR GO; GO:0016020; C:membrane; IEA:InterPro.

DR GO; GO:0005524; F:ATP binding; IEA:InterPro.

DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA:InterPro.

DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.

DR InterPro; IPR000494; EGF_rcpt_L.

DR InterPro; IPR006211; Furin-like.

DR InterPro; IPR006212; Furin_repeat.

DR InterPro; IPR000719; Prot_kinase_core.

DR InterPro; IPR016245; Tyr_kinase_rcpt_EGF/ERB/XmrK.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00757; Furin-like; 1.

DR Pfam; PF07714; Pkinase_Tyr; 1.

DR Pfam; PF01030; Recep_L_domain; 2.

DR PIRSF; PIRSF000619; TyrPK_EGF-R; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00261; FU; 5.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 PE 2: Evidence at transcript level;
 KW Kinase; Receptor.
 SQ SEQUENCE 1319 AA; 146222 MW; D6E487257700A0B2 CRC64;

Query Match 70.0%; Score 245; DB 2; Length 1319;
 Best Local Similarity 70.2%; Pred. No. 1.8e-18;
 Matches 40; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIKHNRRPRDCVAEGKVCDDLCSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGE 57
 ||::|::| | |||||::|: ||||| |||||::| | | | | |
 Db 484 DIRNNKPRGKQQEGKVCDDLCSADGCWGPGPAQLCSLRHYSRRGVCVESCSTQGE 540

RESULT 11

Q5G254_DANRE

ID Q5G254_DANRE Unreviewed; 1429 AA.
 AC Q5G254;
 DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2005, sequence version 1.
 DT 08-APR-2008, entry version 27.
 DE Erbb3.
 GN Name=erbb3b; Synonyms=erbb3;
 OS Danio rerio (Zebrafish) (Brachydanio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15797019; DOI=10.1016/j.cub.2005.02.030;
 RA Lyons D.A., Pogoda H.M., Voas M.G., Woods I.G., Diamond B., Nix R.,
 RA Arana N., Jacobs J., Talbot W.S.;
 RT "erbb3 and erbb2 are essential for schwann cell migration and
 RT myelination in zebrafish."
 RL Curr. Biol. 15:513-524(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Pogoda H.-M., Woods I.G., Talbot W.S.;
 RT "Analysis of the zebrafish erbb3 gene."
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein
 CC kinase family.
 CC -----
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 CC -----
 DR EMBL; AY863052; AAW57896.1; -; mRNA.
 DR RefSeq; NP_001014826.1; -.
 DR UniGene; Dr.81667; -.
 DR Ensembl; ENSDARG00000036993; Danio rerio.
 DR GeneID; 544664; -.

DR KEGG; dre:544664; -.

DR ZFIN; ZDB-GENE-050107-1; erbb3b.

DR GO; GO:0007413; P:axonal fasciculation; IMP:ZFIN.

DR GO; GO:0008347; P:glial cell migration; IMP:ZFIN.

DR GO; GO:0042552; P:myelination; IMP:ZFIN.

DR GO; GO:0048914; P:myelination of anterior lateral line nerve . . .; IMP:ZFIN.

DR GO; GO:0048932; P:myelination of posterior lateral line nerve . . .; IMP:ZFIN.

DR GO; GO:0014044; P:Schwann cell development; IMP:ZFIN.

DR GO; GO:0001964; P:startle response; IMP:ZFIN.

DR InterPro; IPR000494; EGF_rcpt_L.

DR InterPro; IPR006211; Furin-like.

DR InterPro; IPR006212; Furin_repeat.

DR InterPro; IPR000719; Prot_kinase_core.

DR InterPro; IPR016245; Tyr_kinase_rcpt_EGF/ERB/XmrK.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00757; Furin-like; 1.

DR Pfam; PF07714; Pkinase_Tyr; 1.

DR Pfam; PF01030; Recep_L_domain; 2.

DR PIRSF; PIRSF000619; TyrPK_EGF-R; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00261; FU; 3.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

FE 2: Evidence at transcript level;

KW ATP-binding; Nucleotide-binding; Tyrosine-protein kinase.

SQ SEQUENCE 1429 AA; 158993 MW; 081EC5F9E638BA8B CRC64;

Query Match 70.0%; Score 245; DB 2; Length 1429;

Best Local Similarity 69.0%; Pred. No. 1.9e-18;

Matches 40; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIKHNRPRRDCAEAGKVCDDLCSGGCWGPQGLSCRNYSRGGVCVTHCNFLNGEP 58

Db 482 DIKENQKIQICEEEHVCDDLCSAGCWGPQGLSCRNYSRLGTCVSHCNLYSGEP 539

RESULT 12

P79754_FUGRU

ID P79754_FUGRU Unreviewed; 1328 AA.

AC P79754;

DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.

DT 01-AUG-1998, sequence version 2.

DT 08-APR-2008, entry version 50.

DE Erbb3.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontoidea; Tetraodontidae; Takifugu.

OX NCBI_TaxID=31033;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=99177347; PubMed=10077531;

RA Gellner K., Brenner S.;
 RT "Analysis of 148 kb of genomic DNA around the wnt1 locus of Fugu
 RT rubripes.";
 RL Genome Res. 9:251-258(1999).
 CC -|- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein
 CC kinase family.
 CC -----
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 CC -----
 DR EMBL; AF056116; AAC34391.1; -; Genomic_DNA.
 DR HSSP; P21860; 1M6B.
 DR Ensembl; NEWSINFRUG00000149225; Fugu rubripes.
 DR GO; GO:0016020; C:membrane; IEA:InterPro.
 DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA:InterPro.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
 DR InterPro; IPR000494; EGF_rcpt_L.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin_repeat.
 DR InterPro; IPR000719; Prot_kinase_core.
 DR InterPro; IPR016245; Tyr_kinase_rcpt_EGF/ERB/XmrK.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PIRSF; PIRSF000619; TyrPK_EGF-R; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU; 5.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 PE 3: Inferred from homology;
 KW ATP-binding; Nucleotide-binding; Tyrosine-protein kinase.
 SQ SEQUENCE 1328 AA; 148614 MW; A333039258B647E9 CRC64;

Query Match 67.7%; Score 237; DB 2; Length 1328;
 Best Local Similarity 66.7%; Pred. No. 1.4e-17;
 Matches 38; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 2 IKHNRPRRDCVAEGKVCDDLPCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 : ||| :|||:||||| :||||| :||||| :|| :|: :|
 Db 479 LNSNRPMACVADGRVCDPLCSDSGCWGPGPDQCLSCRNYSRHGCTVAGCHFNSGIP 535

RESULT 13

Q4RW26_TETNG

ID Q4RW26_TETNG Unreviewed; 1344 AA.

AC Q4RW26;

DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.

DT 19-JUL-2005, sequence version 1.

DT 08-APR-2008, entry version 18.

DE Chromosome 9 SCAF14991, whole genome shotgun sequence. (Fragment).

```

GN ORFNAMES=GSTENG00028067001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segures B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein
CC kinase family.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; CAAE01014991; CAG07406.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA:InterPro.
DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA:InterPro.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
DR InterPro; IPR000494; EGF_rcpt_L.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR000719; Prot_kinase_core.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.

```


DR SMART; SM00261; FU; 5.
 DE PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 PE 3: Inferred from homology;
 KW ATP-binding; Nucleotide-binding; Tyrosine-protein kinase.
 FT NON_TER 1 1
 SQ SEQUENCE 1344 AA; 148936 MW; 79EFBDCB03B3A1FD CRC64;

Query Match 65.4%; Score 229; DB 2; Length 1344;
 Best Local Similarity 67.3%; Pred. No. 1.2e-16;
 Matches 37; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 2 IKHNRPRRDCVAEGKVCDDLCSGGCWGPGFGQCLSCRNYSRGGVCVTHCNFLNG 56
 : ||| ||||:|:||||| ||||| ||||| ||| | | | : |
 Db 499 LSSNRPLTDCVADGRVCDPLCSDSGCWGPGPDQCLSCRKYSRHGTCTVADCCFFYSG 553

RESULT 14

Q53QS8_HUMAN

ID Q53QS8_HUMAN Unreviewed; 552 AA.
 AC Q53QS8;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 05-FEB-2008, entry version 14.
 DE Putative uncharacterized protein ERBB4 (Fragment).
 GN Name=ERBB4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Cotton M., Spalding L., Nguyen C., McLellan M.;
 RT "The sequence of Homo sapiens BAC clone RP11-541F21.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AC105921; AAY24303.1; -; Genomic_DNA.
 DR UniGene; Hs.390729; -.
 DR SMR; Q53QS8; 1-498.

DR Ensembl; ENSG00000178568; Homo sapiens.
 DR HGNC; HGNC:3432; ERBB4.
 DR ArrayExpress; Q53Q8; -.
 DR GO; GO:0016020; C:membrane; IEA:InterPro.
 DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA:InterPro.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA:InterPro.
 DR InterPro; IPR000494; EGF_rcpt_L.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin_repeat.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR SMART; SM00261; FU; 5.
 PE 2: Evidence at transcript level;
 FT NON_TER 1 1
 FT NON_TER 552 552
 SQ SEQUENCE 552 AA; 61036 MW; BBC7AEDD79ABB536 CRC64;

Query Match 60.6%; Score 212; DB 2; Length 552;
 Best Local Similarity 60.7%; Pred. No. 4.2e-15;
 Matches 34; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 2 IKHNRPRRDCVAEGKVCDCPLSSGGCWGPGGQCLSCRNYSRGGVCVTHCNFLNGE 57
 |: || :| ||| ||: |||| ||||| ||||| :||| :|: || :||
 Db 346 IRDNRKAENCTAEGMVCNHLCSSDGCWGPGPDQCLSCRRFSRGRICIESCNLYDGE 401

RESULT 15

ERBB4_HUMAN

ID ERBB4_HUMAN Reviewed; 1308 AA.
 AC Q15303; Q2M1W1; Q59EW4;
 DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1996, sequence version 1.
 DT 08-APR-2008, entry version 93.
 DE Receptor tyrosine-protein kinase erbB-4 precursor (EC 2.7.10.1)
 DE (p180erbB4) (Tyrosine kinase-type cell surface receptor HER4).
 GN Name=ERBB4; Synonyms=HER4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM JM-A).
 RC TISSUE=Mammary carcinoma;
 RX MEDLINE=93189574; PubMed=8383326;
 RA Plowman G.D., Culouscou J.-M., Whitney G.S., Green J.M., Carlton G.W.,
 RA Foy L., Neubauer M.G., Shoyab M.;
 RT "Ligand-specific activation of HER4/p180erbB4, a fourth member of the
 RT epidermal growth factor receptor family."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS JM-A AND JM-B).

RC TISSUE=Fetal brain;
 RX MEDLINE=97476287; PubMed=9334263; DOI=10.1074/jbc.272.42.26761;
 RA Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,
 RA Klagsbrun M.;
 RT "A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific
 RT tissue distribution and differential processing in response to phorbol
 RT ester.";
 RL J. Biol. Chem. 272:26761-26768(1997).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM JM-A).
 RC TISSUE=Brain;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 RT project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 401-1308 (ISOFORM 3).
 RC TISSUE=Brain;
 RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
 RA Ohara O., Nagase T., Kikuno R.F.;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP INTERACTION WITH DLG2; DLG3; DLG4 AND SNTB2.
 RX MEDLINE=20202681; PubMed=10725395; DOI=10.1073/pnas.070042497;
 RA Garcia R.A., Vasudevan K., Buonanno A.;
 RT "The neuregulin receptor ErbB-4 interacts with PDZ-containing proteins
 RT at neuronal synapses.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:3596-3601(2000).
 RN [6]
 RP INTERACTION WITH MUC1.
 RX PubMed=12939402;
 RA Li Y., Yu W.-H., Ren J., Chen W., Huang L., Kharbanda S., Loda M.,
 RA Kufe D.;
 RT "Heregulin targets gamma-catenin to the nucleolus by a mechanism
 RT dependent on the DF3/MUC1 oncoprotein.";
 RL Mol. Cancer Res. 1:765-775(2003).
 RN [7]
 RP INTERACTION WITH WWOX, DOMAIN, AND MUTAGENESIS OF TYR-1035 AND
 RP TYR-1301.
 RX PubMed=16061658; DOI=10.1158/0008-5472.CAN-05-1150;
 RA Ageilan R.I., Donati V., Palamarchuk A., Trapasso F., Kaou M.,
 RA Pekarsky Y., Sudol M., Croce C.M.;
 RT "WW domain-containing proteins, WWOX and YAP, compete for interaction
 RT with ErbB-4 and modulate its transcriptional function.";
 RL Cancer Res. 65:6764-6772(2005).
 RN [8]
 RP INTERACTION WITH CEFA2T3.
 RX PubMed=16815842; DOI=10.1074/jbc.M60398200;
 RA Linggi B., Carpenter G.;
 RT "ErbB-4 s80 intracellular domain abrogates ETO2-dependent
 RT transcriptional repression.";
 RL J. Biol. Chem. 281:25373-25380(2006).
 RN [9]

RP VARIANTS [LARGE SCALE ANALYSIS] ILE-140 AND TYR-303.

RX PubMed=17344846; DOI=10.1038/nature05610;

RA Greenman C., Stephens P., Smith R., Dalgliesh G.L., Hunter C.,
RA Bignell G., Davies H., Teague J., Butler A., Stevens C., Edkins S.,
RA O'Meara S., Vastrik I., Schmidt E.E., Avis T., Barthorpe S.,
RA Bhamra G., Buck G., Choudhury B., Clements J., Cole J., Dicks E.,
RA Forbes S., Gray K., Halliday K., Harrison R., Hills K., Hinton J.,
RA Jenkinson A., Jones D., Menzies A., Mironenko T., Perry J., Raine K.,
RA Richardson D., Shepherd R., Small A., Tofts C., Varian J., Webb T.,
RA West S., Widaa S., Yates A., Cahill D.P., Louis D.N., Goldstraw P.,
RA Nicholson A.G., Brasseur F., Looijenga L., Weber B.L., Chiew Y.-E.,
RA DeFazio A., Greaves M.F., Green A.R., Campbell P., Birney E.,
RA Easton D.F., Chenevix-Trench G., Tan M.-H., Khoo S.K., Teh B.T.,
RA Yuen S.T., Leung S.Y., Wooster R., Futreal P.A., Stratton M.R.;

RT "Patterns of somatic mutation in human cancer genomes.";

RL Nature 446:153-158(2007).

CC -!- FUNCTION: Specifically binds and is activated by neuregulins, NRG-
CC 2, NRG-3, heparin-binding EGF-like growth factor, betacellulin and
CC NTAK. Interaction with these factors induces cell differentiation.

CC Not activated by EGF, TGF-A, and amphiregulin.

CC -!- CATALYTIC ACTIVITY: ATP + a [protein]-L-tyrosine = ADP + a
CC [protein]-L-tyrosine phosphate.

CC -!- SUBUNIT: Homodimer or heterodimer with each of the other ERBB
CC receptors (Potential). Interacts with PDZ domains of DLG2, DLG3,
CC DLG4 and the syntrophin SNTB2. Interacts with CBFA2T3, MUC1 and
CC WWOX.

CC -!- INTERACTION:
CC P78352:DLG4; NbExp=3; IntAct=EBI-80371, EBI-80389;
CC P00533:EGFR; NbExp=2; IntAct=EBI-80371, EBI-297353;
CC P04626:ERBB2; NbExp=2; IntAct=EBI-80371, EBI-641062;
CC P21860:ERBB3; NbExp=2; IntAct=EBI-80371, EBI-720706;
CC Q05586:GRIN1; NbExp=1; IntAct=EBI-80371, EBI-998542;

CC -!- SUBCELLULAR LOCATION: Membrane; Single-pass type I membrane
CC protein.

CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=The 2 isoforms differ functionally in their response to
CC phorbol ester: isoform JM-A is processed but not isoform JM-B.
CC So, they respectively represent cleavable and non-cleavable
CC forms of the receptor. Both isoforms are expressed in
CC cerebellum, but only the isoform JM-B is expressed in the heart;
CC Name=JM-A;
CC IsoId=Q15303-1; Sequence=Displayed;
CC Name=JM-B;
CC IsoId=Q15303-2; Sequence=VSP_002895;
CC Name=3;
CC IsoId=Q15303-3; Sequence=VSP_022148;

CC -!- TISSUE SPECIFICITY: Expressed at highest levels in brain, heart,
CC kidney, in addition to skeletal muscle, parathyroid, cerebellum,
CC pituitary, spleen, testis and breast. Lower levels in thymus,
CC lung, salivary gland, and pancreas.

CC -!- DOMAIN: The WW-binding motifs mediate interaction with WWOX.

CC -!- PTM: Ligand binding increases phosphorylation on tyrosine
CC residues.

```

CC      -!- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein
CC      kinase family. EGF receptor subfamily.
CC      -!- SIMILARITY: Contains 1 protein kinase domain.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; L07868; AAB59446.1; -; mRNA.
DR      EMBL; BC112199; AAI12200.1; -; mRNA.
DR      EMBL; AB209697; BAD92934.1; -; mRNA.
DR      PIR; A47253; A47253.
DR      RefSeq; NP_001036064.1; -.
DR      RefSeq; NP_005226.1; -.
DR      UniGene; Hs.390729; -.
DR      PDB; 2AHX; X-ray; 2.40 A; A/B=26-641.
DR      PDBsum; 2AHX; -.
DR      DIP; DIP:6094N; -.
DR      IntAct; Q15303; -.
DR      PhosphoSite; Q15303; -.
DR      Ensembl; ENSG00000178568; Homo sapiens.
DR      GeneID; 2066; -.
DR      KEGG; hsa:2066; -.
DR      H-InvDB; HIX0030012; -.
DR      HGNC; HGNC:3432; ERBB4.
DR      HPA; CAB000276; -.
DR      MIM; 600543; gene.
DR      PharmGKB; PA27847; -.
DR      ArrayExpress; Q15303; -.
DR      CleanEx; HS_ERBB4; -.
DR      GermOnline; ENSG00000178568; Homo sapiens.
DR      GO; GO:0016323; C:basolateral plasma membrane; IDA:UniProtKB.
DR      GO; GO:0005887; C:integral to plasma membrane; TAS:ProtInc.
DR      GO; GO:0046982; F:protein heterodimerization activity; IDA:UniProtKB.
DR      GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; TAS:ProtInc.
DR      GO; GO:0008283; P:cell proliferation; TAS:ProtInc.
DR      GO; GO:0007275; P:multicellular organismal development; TAS:ProtInc.
DR      GO; GO:0007165; P:signal transduction; IDA:UniProtKB.
DR      InterPro; IPR000494; EGF_rcpt_L.
DR      InterPro; IPR006211; Furin-like.
DR      InterPro; IPR006212; Furin_repeat.
DR      InterPro; IPR000719; Prot_kinase_core.
DR      InterPro; IPR016245; Tyr_kinase_rcpt_EGF/ERB/XmrK.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      InterPro; IPR008266; Tyr_pkinase_AS.
DR      InterPro; IPR004019; YLP_motif.
DR      Pfam; PF00757; Furin-like; 1.
DR      Pfam; PF07714; Pkinase_Tyr; 1.
DR      Pfam; PF01030; Recep_L_domain; 2.
DR      Pfam; PF02757; YLP; 2.
DR      PIRSF; PIRSF000619; TyrPK_EGF-R; 1.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00261; FU; 5.
DR      SMART; SM00219; TyrKc; 1.

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DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 PE 1: Evidence at protein level;
 KW 3D-structure; Alternative splicing; ATP-binding; Glycoprotein; Kinase;
 KW Membrane; Nucleotide-binding; Phosphoprotein; Polymorphism; Receptor;
 KW Repeat; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 1308 Receptor tyrosine-protein kinase erbB-4.
 FT /FTId=PRO_0000016674.
 FT TOPO_DOM 26 651 Extracellular (Potential).
 FT TRANSMEM 652 675 Potential.
 FT TOPO_DOM 676 1308 Cytoplasmic (Potential).
 FT DOMAIN 718 985 Protein kinase.

Query Match 60.6%; Score 212; DB 1; Length 1308;
 Best Local Similarity 60.7%; Pred. No. 9.4e-15;
 Matches 34; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 2 IKHNRRPRDCVAEGKVC DPLCSSGGCWGPGGQCLSCRNYSRGGVCVTHCNFLNGE 57
 |: || :| ||| ||: |||| ||||| ||||| :||| :|: || :||
 Db 487 IRDNRKAENCTAEGMVCNHLCSSDGCWGPGPDQCLSCRRFSRGRICIESCNLYDGE 542

Search completed: November 12, 2008, 12:14:39

Job time : 224 secs

SCORE 1.9